AMENDMENT

Kindly amend the application, without prejudice, without admission, without surrender of subject matter, and without any intention of creating any estoppel as to equivalents as follows:

IN THE SPECIFICATION:

Kindly amend the specification, without prejudice, without admission, without surrender of subject matter, and without any intention of creating any estoppel as to equivalents as follows:

Page 33, lines 718-727, please rewrite the paragraph thereat as follows:

In the context of the present invention, a homologous sequence is taken to include an amino acid sequence which is at least 75, 85 or 90% identical, preferably at least 95 or 98% identical at the amino acid level over at least, for example, the amino acid sequence as set out in SEQ ID No 22 of the sequence listing herein. In particular, homology should typically be considered with respect to those regions of the sequence known to be essential for enzyme activity rather than non-essential neighbouring sequences. These regions include but are not limited to the putative FAD binding domains in HOX such as $SGGH_{79}C$ (residues 76-80 of SEQ ID NO: 23), $LGGH_{146}I$ (residues 143-147 of SEQ ID NO: 23) and $LGGH_{320}A$ (residues 317-321 of SEQ ID NO: 23). Although homology can also be considered in terms of similarity (i.e. amino acid residues having similar chemical properties/functions), in the context of the present invention it is preferred to express homology in terms of sequence identity.

Page 43, lines 978-979, please rewrite the paragraph thereat as follows:

Figure 5 provides the individual oligonucleotides used to synthesize the HOX gene with codon optimization (SEQ ID NOS 2-21, respectively in order of appearance).

Page 43, lines 980-981, please rewrite the paragraph thereat as follows:

Figure 6 provides a nucleotide sequence of the synthetic HOX gene (SEQ ID NO: 22) and the corresponding amino acid sequence (SEQ ID NO: 23).

Page 52, lines 1185-1190 and Table 1, please rewrite the paragraph and table thereat as follows:

Table 1 shows the various HOX/secretion fusion constructs which were inserted as Eco RI/Not I blunt fragments into the multiple cloning site of the *H. polymorpha* expression/integration vector. The different signal sequences were derived from the glucoamylase gene from *Schwanniomyces occidentalis,* α-factor mating type gene from *Saccharomyces cerevisiae* and the TAKA-amylase from *Aspergillus oryzae.* A NcoI/NotI HOX construct without a signal sequence was also cloned into the vector.

Name of Clone	signal sequence	HOX	Fusion junction
1. DK 1	glucoamylase	wildtype synthetic	SAIQA MATLP (SEQ ID NOS 24 and 25)
2. DK 2	glucoamylase	wildtype synthetic	SAIQA ATLP (SEQ ID NOS 24 and 26)
3. DK 3	α-factor	wildtype synthetic	KREAEA MATLP (SEQ ID NOS 27 and 25)
4. DK 4	α-factor	wildtype synthetic	KREAEA ATLP (SEQ ID NOS 27 and 26)
5. DK 5	α-factor	mutant synthetic	KREAEA MATLP (SEQ ID NOS 27 and 25)
6. DK 6	α-factor	mutant synthetic	KR MATLP (SEQ ID NO: 25)
7. DK 7	TAKA amylase	mutant synthetic	APALA MATLP (SEQ ID NOS 28 and 25)
8. DK 8	No signal sequence	wild type synthetic	none - MATLP (SEQ ID NO: 25)

Table 1. The term mutant synthetic relates to a putative KEX 2 protease cleavage site R_{331}-K_{332} to R_{331}-P_{332}.

Page 98, lines 1939-1944, please rewrite the paragraphs thereat as follows:

The glucan lyase gene is assembled using PCR using the following primers

(SEQ ID NO: 29)

US-agl1: GAA TTC ATG ACC GCA TTG TCC GAC AAA CAA ACG GCT

(SEQ ID NO: 30)

LS-agl2: ACC CGG GGT AGA AGA GCC GGC AGC AAA CCA GTT

(SEQ ID NO: 31)

US-agl5: GGG TGA GCT CTG CCA CTT CCA GGG CTG CGC TGT TC

(SEQ ID NO: 32)

LS-agl6: GGA GAT CTT TAT TAA TGG TGA TGG TGA TGG TGG GTA ATT GTG ATC ACA GCG TCC GG

Page 101, lines 2003-2012, please rewrite the paragraph thereat as follows:

In a PCR tube 10 µl of cell-free extract is mixed with 50 pmole of primers, 1 µl of each dNTP, 10 µl of AmpliTaq DNA Polymerase Buffer, 1 U of AmpliTaq DNA Polymerase and water to a final volume of 50 µl. After preheating for 30 seconds at 95°C the PCR-program consisted in 30 cycles of 95°C for 30 seconds, 55°C for 1 minute and 68°C for 2 minutes and 5 minutes at 72°C extension at the end. The PCR products are loaded on 2% agarose gels to check the size of the products. The two primers US3-aglcore and LS4-aglcore are used for the PCR-screening

(SEQ ID NO: 33)

US3-aglcore: GGA GAT ACT ACC TGG AAC TCT GGA CAA GAG GAC

(SEQ ID NO: 34)

LS4-aglcore: GTT TGG ATC CCC GCC AGT ACC CAC

Page 109, lines 2174-2177 and the following table, please rewrite the paragraph and table thereat as follows:

The N-terminal sequencing of the purified glucan lyase resulted in a sequence of 20 amino acids (GSTDNPDGIDYKTYDYV GVW) (SEQ ID NO: 35) that was 100% identical with the wild type algal glucan lyase (See Table 21 below). Surprisingly the glucan lyase from *H. polymorpha* is very active even though the N-terminal is 11 amino acids shorter than the wild type protein.

	N-terminal sequence
Wild type glucan lyase (SEQ ID NO: 36)	TALSDKQTATAGSTDNPDGIDYKTYDYVGVW
Algal glucan lyase from H. Polymorpha (SEQ ID NO: 35)	GSTDNPDGIDYKTYDYVGVW

Kindly replace the previously filed sequence listing with the enclosed papers entitled --Sequence Listing--.